```
1   GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
    CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

73  GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
    CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145 GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
    CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
    GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
1                                   MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
    GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
16  LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
    TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
40  LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
    GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
64  ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
    GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
88  GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
    GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG. 1A

```
649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATTGCATACG
     CCCGGGGGGGTC TCGGGAGGTTTG TAGATGATGTGT AGCTAAAGACAC AACCTCACCGGG TATAACGTATGC
328  GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTrpPro IleLeuHisThr
```

FIG. 1B

```
1297  ATACAACTGTTT TTCATGCGATCC AAGTGCTCCCGT GTCACTACATTC TTATTTCCTGTG CAAGTTATTACG
      TATGTTGACAAA AAGTACGCTAGG TTCACGAGGGCA CAGTGATGTAAG AATAAAGGACAC GTTCAATAATGC
 352  IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr

1369  ACATCGACTTGC CGGATGACTTCA TTTAGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGAGCACAG
      TGTAGCTGAACG GCCTACTGAAGT AAATCGAAATGG TGGGACTTGGGT AGGTACGTCCGG ACGTCTCGTGTC
 376  ThrSerThyCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln

1441  ATGGGGGAATTC CGAATCAGATGG TGTTTCTGGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTGTG
      TACCCCCTTAAG GCTTAGTCTACC ACAAAGACCCCC CTGTCCTAGGAC CCATGCCGAGAC AAACACGAACAC
 400  MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal

1513  CTTATTCTTCTT CTTGGGAGGCTG AATATGCATCAG ACGACACTGCTC CGGCAACGGGCC AGTGTGGAGGCG
      GAATAAGAAGAA GAACCCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTTGCCCGG TCACACCTCCGC
 424  LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla

1585  GAAGCCGGCCAG CATGGTCCCCTG TGATAGGATTGA AAGAGCTACTGA GAATAGGGGGCT TCTCAATGAGAG
      CTTCGGCCGGTC GTACCAGGGGAC ACTATCCTAACT TTCTCGATGACT CTTATCCCCCGA AGAGTTACTCTC
 448  GluAlaGlyGln HisGlyProLeu (SEQ ID NO: 2)

1657  AGCGGAGGCTGC TGTTATCATGGG AACCAGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
      TCGCCTCCGACG ACAATAGTACCC TTGGTCCGTCTA GTTAGTAGGGAC CGTCCAGTCCGT CCTTCAATGAAT

1729  GCTTCTCCTTCA CCTTCTTCCCAC AGAATTTATTAT AGGCTTGTTCCA AGTTGTAGTGTG TGATCAGATTCG
      CGAAGAGGAAGT GGAAGAAGGGTG TCTTAAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC

1801  TGCTGCCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAATTC GATATCAAGCTT ATCGATACCGTC
      ACGACGGACAGT CGAGACACGATG GACCGTCAAGGG GAGTACCTTAAG CTATAGTTCGAA TAGCTATGGCAG

1873  GACCT (SEQ ID NO: 1)
      CTGGA
```

FIG. 1C

FIG. 1

FIG. 1A
FIG. 1B
FIG. 1C

```
1   GNTCTAGAANTA GTGGATCCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGGAAGGGCTC TGGTGGGGCTGA
    CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCCTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCCGACT

73  GCGCTCTGCCGC GGGGGCGCGGGC ACAGCAGGAAGC AGGTCCGCGTGG GCGCTGGGGGCA TCAGCTACCGGG
    CGCGAGACGGCG CCCCCGCGCCCG TGTCGTCCTTCG TCCAGGCGCACC CGCGACCCCCGT AGTCGATGGCCC

145 GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGGCAGC CACCCCGGGGGG TGGGCGACTTTG GGGGAGTTGGTG
    CACCAGGCCCGA CTTCTCGGTCCG TCGGTTCCGTCG GTGGGGCCCCCC ACCCGCTGAAAC CCCCTCAACCAC

217 CCCCGCCCCCCA GGCCTTGGCGGG GTCATGGGGCCC CCCCATTCTGGG CCGGGGGGCGTG CGAGTCGGGGCC
    GGGGCGGGGGGT CCGGAACCGCCC CAGTACCCCGGG GGGGTAAGACCC GGCCCCCCGCAC GCTCAGCCCCGG
1                                  MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289 CTGCTGCTGCTG GGGGTTTTGGGG CTGGTGTCTGGG CTCAGCCTGGAG CCTGTCTACTGG AACTCGGCGAAT
    GACGACGACGAC CCCCAAAACCCC GACCACAGACCC GAGTCGGACCTC GGACAGATGACC TTGAGCCGCTTA
16  LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361 AAGAGGTTCCAG GCAGAGGGTGGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
    TTCTCCAAGGTC CGTCTCCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGAGACGGGG
40  LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433 CGGGCCCGGCCT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACCTG GTAGGGGGTGCT
    GCCCGGGCCGGA GGACCGGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCGACATGGAC CATCCCCCACGA
64  ArgAlaArgPro ProGlyProHis SerSerProAsn TryGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505 CAGGGCCGGCGC TGTGAGGCACCC CCTGCCCCAAAC CTCCTTCTCACT TGTGATCGCCCA GACCTGGATCTC
    GTCCCGGCCGCG ACACTCCGTGGG GGACGGGGTTTG GAGGAAGAGTGA ACACTAGCGGGT CTGGACCTAGAG
88  GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577 CGCTTCACCATC AAGTTCCAGGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCGCTCG CACCACGATTAC
    GCGAAGTGGTAG TTCAAGGTCCTC ATATCGGGATTA GAGACCCCGGTG CTCAAGGCGAGC GTGGTGCTAATG
112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr
```

FIG. 2A

```
649  TACATCATTGCC ACATCGGATGGG ACCCGGGAGGGC CTGGAGAGCCTG CAGGGAGGTGTG TGCCTAACCAGA
     ATGTAGTAACGG TGTAGCCTACCC TGGGCCCTCCCG GACCTCTCGGAC GTCCCTCCACAC ACGGATTGGTCT
136  TyrIleIleAla ThrSerAspGly ThrArgGluGly LeuGluSerLeu GlnGlyGlyVal CysLeuThrArg

721  GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCCC CGAGGAGGGGCT GTCCCCCGAAAA CCTGTGTCTGAA
     CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCCTCCCCGA CAGGGGCTTTT GGACACAGACTT
160  GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu

793  ATGCCCATGGAA AGAGACCGAGGG GCAGCCCACAGC CTGGAGCCTGGG AAGGAGAACCTG CCAGGTGACCCC
     TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTCG GACCTCGGACCC TTCCTCTTGGAC GGTCCACTGGGG
184  MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluAsnLeu ProGlyAspPro

865  ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGGCCCC CTGCCCCCTCCC AGCATGCCTGCA GTGGCTGGGGCA
     TGGTCGTTACGT TGGAGGGCCCCA CGACTTCCGGGG GACGGGGGAGGG TCGTACGGACGT CACCGACCCCGT
208  ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla

937  GCAGGGGGGCTG GCGCTGCTCTTG CTGGGCGTGGCA GGGGCTGGGGGT GCCATGTGTTGG CGGAGACGGCGG
     CGTCCCCCCGAC CGCGACGAGAAC GACCCGCACCGT CCCCGACCCCCA CGGTACACAACC GCCTCTGCCGCC
232  AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg

1009 GCCAAGCCTTCG GAGAGTCGCCAC CCTGGTCCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGGT
     CGGTTCGGAAGC CTCTCAGCGGTG GGACCAGGACCG AGGAAGCCCTCC CCTCCCAGAGAC CCGGACCCCCCA
256  AlaLysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly

1081 GGAGGTGGGATG GGACCTCGGGAG GCTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGGT GGCGGGGCTGCA
     CCTCCACCCTAC CCTGGAGCCCTC CGACTCGGACCC CTCGATCCCTAT CGAGACGCCCCA CCGCCCCGACGT
280  GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla

1153 GATCCCCCCTTC TGCCCCCACTAT GAGAAGGTGAGT GGTGACTATGGG CATCCTGTGTAT ATCGTGCAGGAT
     CTAGGGGGGAAG ACGGGGGTGATA CTCTTCCACTCA CCACTGATACCC GTAGGACACATA TAGCACGTCCTA
304  AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp

1225 GGGCCCCCCCAG AGCCCTCCAAAC ATCTACTACAAG GTATGAGGGCTC TTGGAGTGGCCC ATATTGCATACG
     CCCGGGGGGGGTC TCGGGAGGTTTG TAGATGATGTTC CATACTCCCGAG AACCTCACCGGG TATAACGTATGC
328  GlyProProGln SerProProAsn IleTyrTyrLys ValOP*  (SEQ ID NO: 4)
```

FIG. 2B

```
1297  AGCCCTTCTTGG GGTGCTCCTCCA GTTTAATTCCTG GTTTGAGGGACA CCTCTAACATCT CGGCCCCCTGTG
      TCGGGAAGAACC CCACGAGGAGGT CAAATTAAGGAC CAAACTCCCTGT GGAGATTGTAGA GCCGGGGGACAC

1369  CCCCCCCAGCCC CTTCACTCCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCCTT AGGATTCCCACT
      GGGGGGGTCGGG GAAGTGAGGAGG GCCGACGACAGG AGCAGAGGTGAA AATCCTAAGGAA TCCTAAGGGTGA

1441  GCCCCACTTCCT GCCCTCCCGTTT GGCCATGGGTGC CCCCCTCTGTCT CAGTGTCCCTGG ATCCTTTTTCCT
      CGGGGTGAAGGA CGGGAGGGCAAA CCGGTACCCACG GGGGGAGACAGA GTCACAGGGACC TAGGAAAAAGGA

1513  TGGGGAGGGGCA CAGGCTCAGCCT CCTCTCTGACCA TGACCCAGGCAT CCTTGTCCCCCT CACCCACCCAGA
      ACCCCTCCCCGT GTCCGAGTCGGA GGAGAGACTGGT ACTGGGTCCGTA GGAACAGGGGGA GTGGGTGGGTCT

1585  GCTAGGGGCGGG AACAGCCCACCT TTTGGTTGGCAC CGCCTTCTTTCT GCCTCTCACTGG TTTTCTCTTCTC
      CGATCCCCGCCC TTGTCGGGTGGA AAACCAACCGTG GCGGAAGAAAGA CGGAGAGTGACC AAAAGAGAAGAG

1657  TATCTCTTATTC TTTCCCTCTCTT CCGTCTCTAGGT CTGTTCTTCTTC CCTAGCATCCTC CTCCCCACATCT
      ATAGAGAATAAG AAAGGGAGAGAA GGCAGAGATCCA GACAAGAAGAAG GGATCGTAGGAG GAGGGGTGTAGA

1729  CCTTTCACCCTC TTGGCTTCTTAT CCTGTGCCTCTC CCATCTCCTGGG TGGGGGCATCAA AGCATTTCTCCC
      GGAAAGTGGGAG AACCGAAGAATA GGACACGGAGAG GGTAGAGGACCC ACCCCCGTAGTT TCGTAAAGAGGG

1801  CTTAGCTTTCAG CCCCCCTTCTGA CCTCTCATACCA ACCACTCCCCTC AGTCTGCCAAAA ATGGGGGCCTTA
      GAATCGAAAGTC GGGGGGAAGACT GGAGAGTATGGT TGGTGAGGGGAG TCAGACGGTTTT TACCCCCGGAAT

1873  TGGGGAAGGCTC TGACACTCCACC CCAGCTCAGGCC ATGGGCACCAGG GCTCCATTCTCT GGCCTGGCCCAG
      ACCCCTTCCGAG ACTGTGAGGTGG GGTCGAGTCCGG TACCCGTCGTCC CGAGGTAAGAGA CCGGACCGGGTC

1945  GCCTCTACATAC TTACTCCAGCCA TTTGGGGTGGTT GGGTCATGACAG CTACCATGAGAA GAAGTGTCCCGT
      CGGAGATGTATG AATGAGGTCGGT AAACCCCACCAA CCCAGTACTGTC GATGGTACTCTT CTTCACAGGGCA

2017  TTTGTCCSGTGG CCAATAGCAAGA TATGAACCGGTC GGGACATGTATG GACTTGGTCTGA TGCTGAATGGGC
      AAACAGGTCACC GGTTATCGTTCT ATACTTGGCCAG CCCTGTACATAC CTGAACCAGACT ACGACTTACCCG
```

FIG. 2C

2089 CACTTGGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCCC GGACAGAAATGG CCTGGGAAGTAG
GTGAACCCTGGC CTTCACTGAACG AGGTCTGTTCTC CACTGGTCCGGG CCTGTCTTTACC GGACCCTTCATC

2161 CAGAAGCAGTGC AGCAGGAACTGG AAGTGCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AAACAGGAAGTG
GTCTTCGTCACG TCGTCCTTGACC TTCACGGAAGTA GGTCCTGTCCTT CATCGTGAAGAC TTTGTCCTTCAC

2233 GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGGA TCAGGAGGTGGG AGGTGGATGGTT CTTATTCTGTGG
CAGACCGACCTT GAGGTTCACCGA ATCAGACCCCCT AGTCCTCCACCC TCCACCTACCAA GAATAAGACACC

2305 AGAAGAAGGGCG GGAAGAACTTCC TTTCAGGAGGAA GCTGGAACTTAC TGACTGTAAGAG GTTAGAGGTGGA
TCTTCTTCCCGC CCTTCTTGAAGG AAAGTCCTCCTT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT

2377 CCGA **(SEQ ID NO: 3)**
GGCT

FIG. 2D

FIG. 2

- FIG. 2A
- FIG. 2B
- FIG. 2C
- FIG. 2D

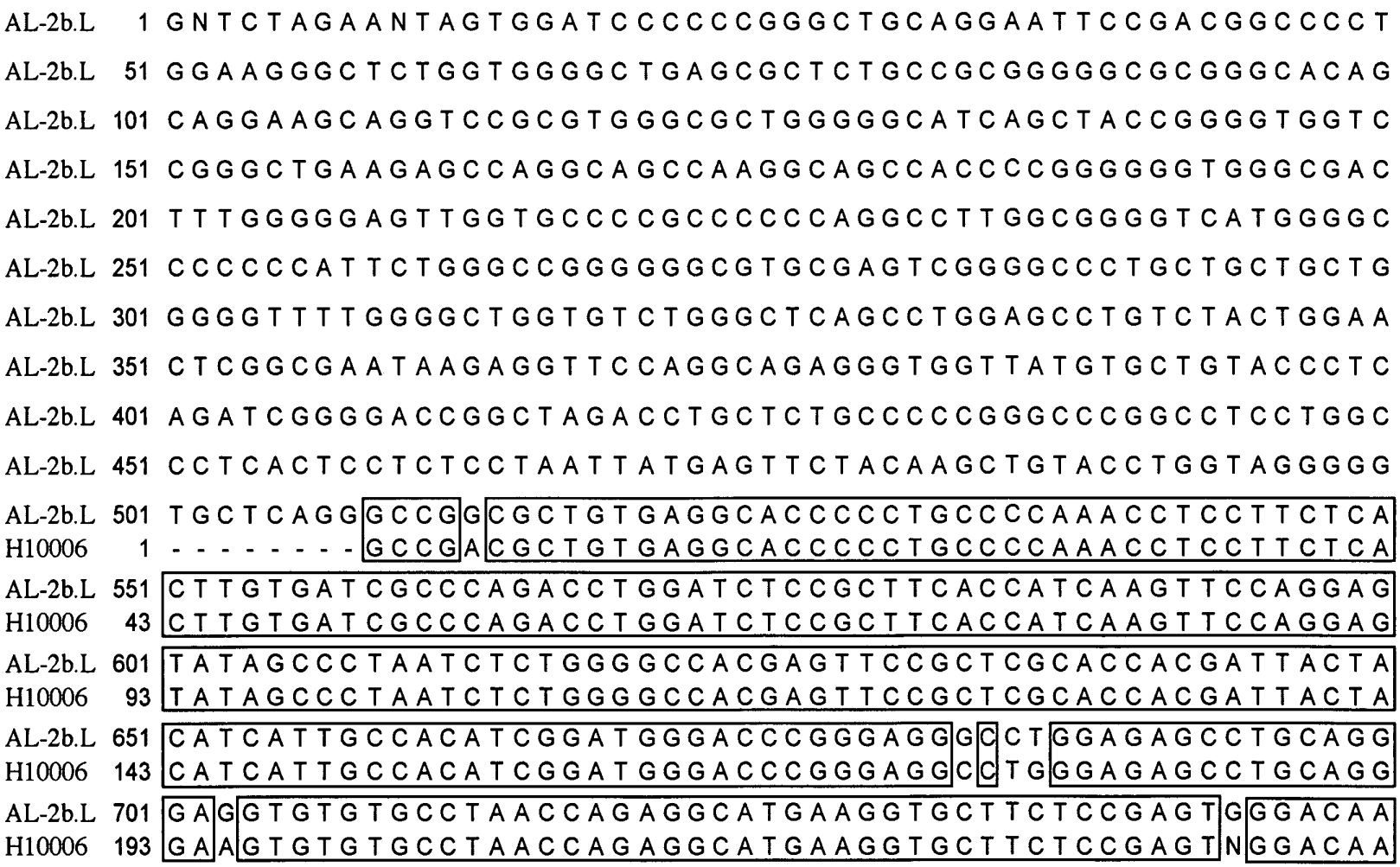
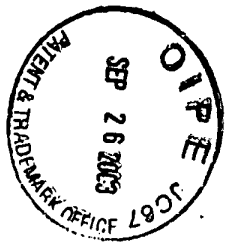


FIG. 3A




```
AL-2b.L  751 AGTCCCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT
H10006   243 AGT-CCCGAGGAGGGGCTGTCCCCCGAAAACCTGTGTCTGAAATGCCCAT

AL-2b.L  801 GGAAAGAGACCGAGGGGCAGCCCACAGCCT-GGAGCCT-GGGAAGGAGAA
H10006   292 GGAAAGAGACCGAGGGGCAGCCCACAGCCTGGGAGCCTGGGAAGGAGAA

AL-2b.L  849 CCTGCCAGGTGACCCCACCAGCAATGCAACCTCCCGGGGT--GCTGAAGG
H10006   342 CCTGCCAGGTGACCCCACCAGCAATNCAACCTTCCGGGGTTGCTTGAAGG

AL-2b.L  897 CCCCCT--GCCCCCTCCCAGCA-TGCCTGCAGT--GGCTGGGGCAGCAGG
H10006   392 GCCCCTTGACCCTTTCCCAGCATTGCNTGCANTTGGTTNGGGGCAGCANG

AL-2b.L  942 GGGGC----TGGCGCTGCTCTTGCTGGGCGTGGCAGGGGCTGGGGGTGCC
H10006   442 GGGGNGTTTTGGC (SEQ ID NO: 5)

AL-2b.L  988 ATGTGTTGGCGGAGACGGCGGGCCAAGCCTTCGGAGAGTCGCCACCCTGG

AL-2b.L 1038 TCCTGGCTCCTTCGGGAGGGGAGGGTCTCTGGGCCTGGGGGGTGGAGGTG

AL-2b.L 1088 GGATGGGACCTCGGGAGGCTGAGCCTGGGGAGCTAGGGATAGCTCTGCGG

AL-2b.L 1138 GGTGGCGGGGCTGCAGATCCCCCCTTCTGCCCCCACTATGAGAAGGTGAG

AL-2b.L 1188 TGGTGACTATGGGCATCCTGTGTATATCGTGCAGGATGGGCCCCCCCAGA

AL-2b.L 1238 GCCCTCCAAACATCTACTACACATCGATTTCTGTGTTGGAGTGGCCCATA

AL-2b.L 1288 TTGCATACGATACAACTGTTTTTCATGCGATCCAAGTGCTCCCGTGTCAC
```

FIG. 3B

AL-2b.L 1338 TACATTCTTATTTCCTGTGCAAGTTATTACGACATCGACTTGCCGGATGA
AL-2b.L 1388 CTTCATTTAGCTTTACGACCCTGAACCCATCCATGCAGGCCTGCAGAGCA
AL-2b.L 1438 CAGATGGGGGAATTCCGAATCAGATGGTGTTTCTGGGGGGACAGGATCCT
AL-2b.L 1488 GGGTACGGCTCTGTTTGTGCTTGTGCTTATTCTTCTTCTTGGGAGGCTGA
AL-2b.L 1538 ATATGCATCAGACGACAGTGCTCCGGCAACGGGCCAGTGTGGAGGCGGAA
AL-2b.L 1588 GCCGGCCAGCATGGTCCGCTGTGATAGGATTGAAAGAGCTACTGAGAATA
AL-2b.L 1638 GGGGGCTTCTCAATGAGAGAGCGGAGGCTGCTGTTATCATGGGAACCAGG
AL-2b.L 1688 CAGATCAATCATCCCTGGCAGQTCAGGCAGGAAGTTACTTAGCTTCTCCT
AL-2b.L 1738 TCACCTTCTTCCCACAGAATTTATTATAGGCTTGTTCCAAGTTGTAGTGT
AL-2b.L 1788 GTGATCAGATTCGTGCTGCCTGTCAGCTCTGTGCTACCTGGCAGTTCCCC
AL-2b.L 1838 TCATGGAATTCGATATCAAGCTTATCGATACCGTCGACCT **(SEQ ID NO: 1)**

FIG. 3C

FIG. 3

FIG. 3A
FIG. 3B
FIG. 3C


```
lerk2      1 MA-RPGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKG
huHTKL     1 MAVRRDSVWKYCWGVLMV---LCRTAISKSIVLEPIYWNSSNSKFLPGQG
AL2.sht    1 MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG
AL2.long   1 MG-PPHSGPGGVRVGALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGG

lerk2     50 LVIYPKIGDKLDIICPRA---EAGR--PYEYYKLYLVRPEQAAACSTVLD
huHTKL    48 LVLYPQIGDKLDIICPKV---DSKTVGQYEYYKVYMVDKDQADRCTIKKE
AL2.sht   48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA
AL2.long  48 YVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPA

lerk2     95 PNVLVTCNRPEQEIRFTIKFQEFSPNYMGLEFKKHHDYYITSTSNGSLEG
huHTKL    95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNGSLEG
AL2.sht   98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG
AL2.long  98 PNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREG

lerk2    145 LENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQ
huHTKL   145 LDNQEGGVCQTRAMKILMKVGQDASS-----AGSTRNKDPTRRPELEAG
AL2.sht  148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
AL2.long 148 LESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLE
```

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FIG. 4A

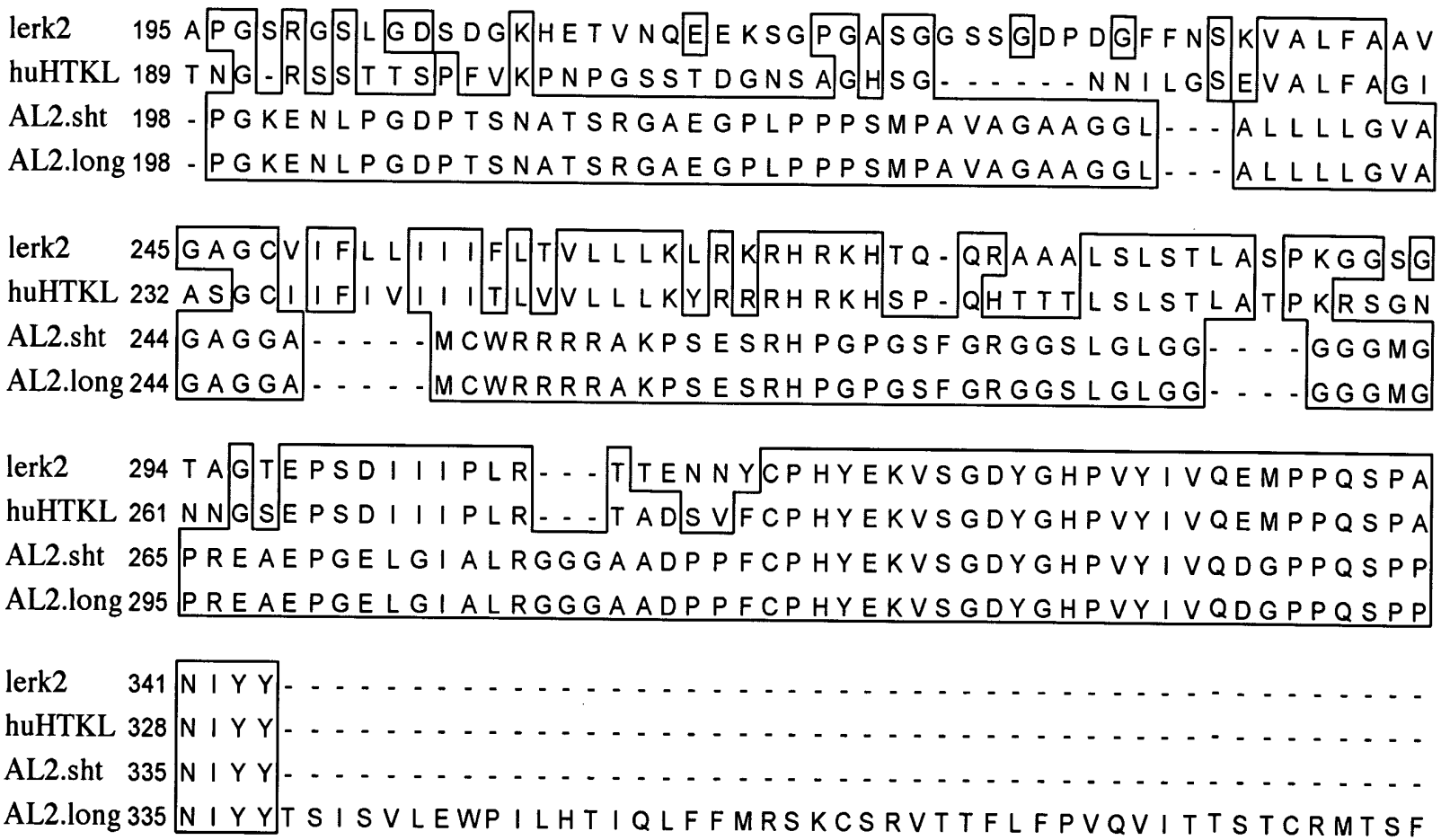

FIG. 4B

lerk2 345 - K V - - - - - - - - - - (SEQ ID NO: 9)

huHTKL 332 - K V - - - - - - - - - - (SEQ ID NO: 10)

AL2.sht 339 - K V - - - - - - - - - - (SEQ ID NO: 4)

AL2.long 385 S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L L G R L N M H

AL2.long 435 Q T T L L R Q R A S V E A E A G Q H G P L (SEQ ID NO: 2)

FIG. 4C

FIG. 4A

FIG. 4B

FIG. 4C

FIG. 4

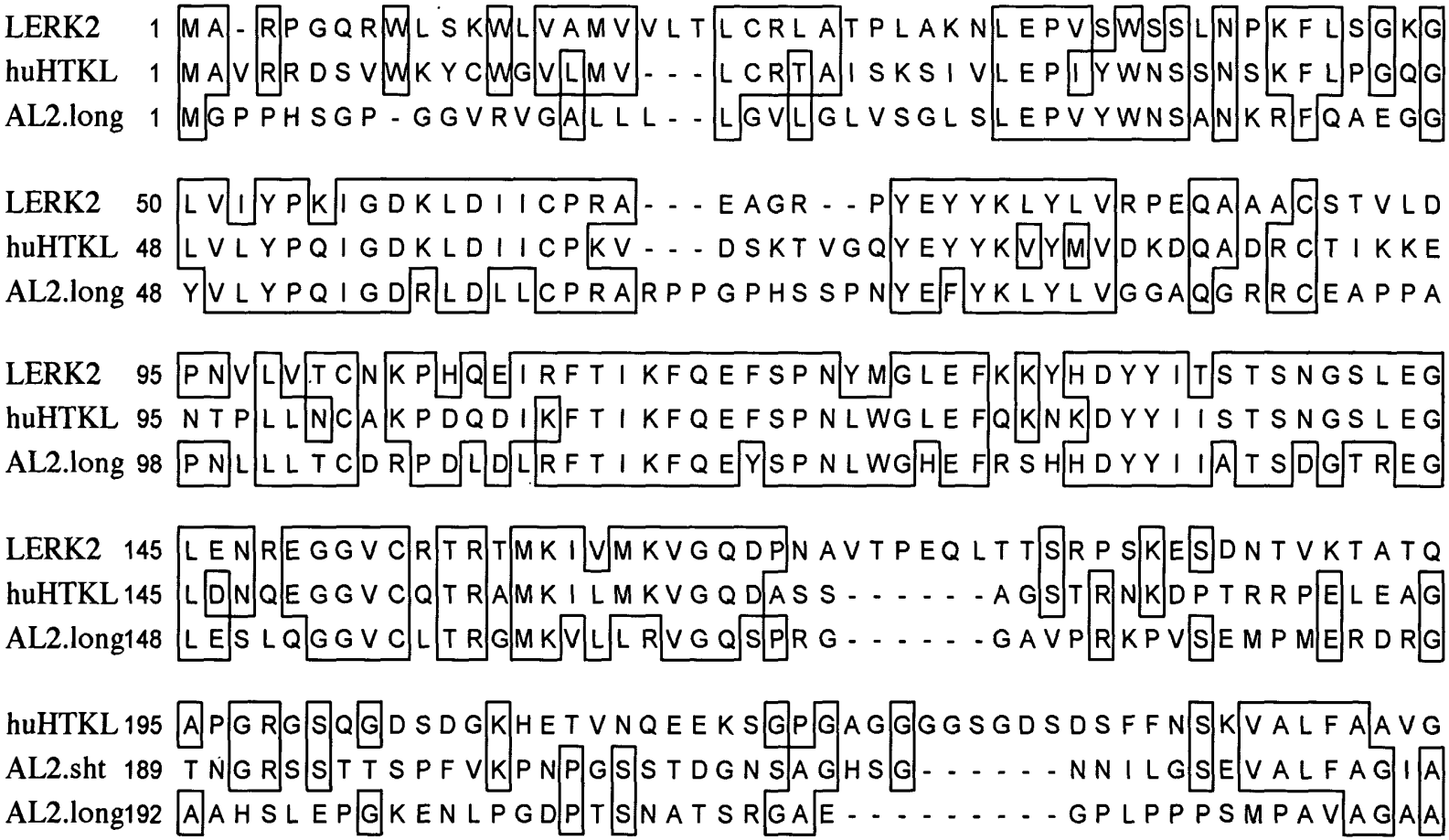

FIG. 5A

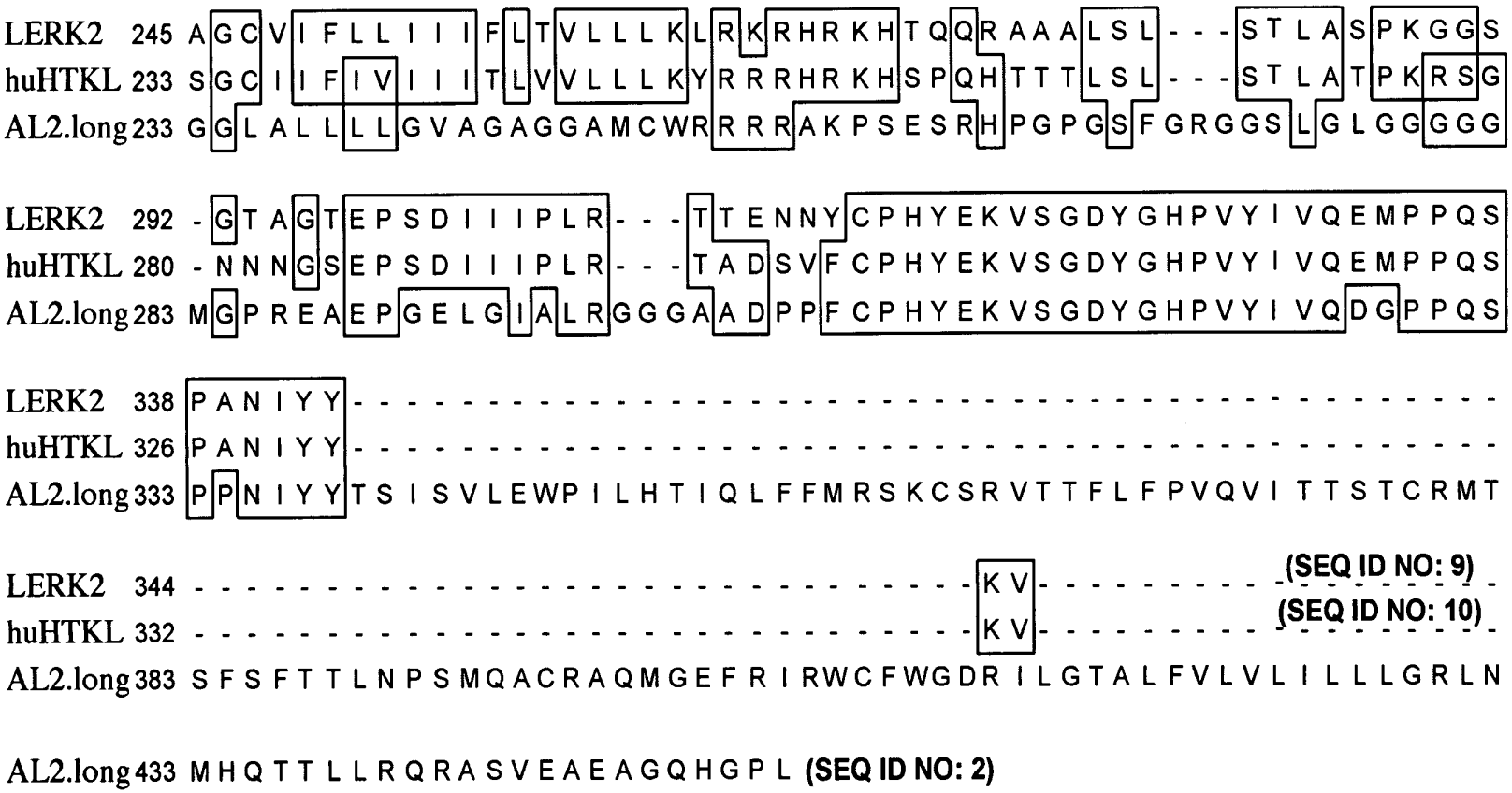

FIG. 5B

FIG. 5

FIG. 5A

FIG. 5B